# Roles of Mammalian Coro1B in Actin Dynamics and Cell Migration


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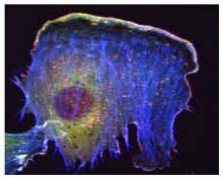
## BACKGROUND

Cell migration is a highly integrated multi-step process that orchestrates embryonic morphogenesis; contributes to tissue repair and regeneration; takes part in immune response and neuron development; and drives disease progression in cancer, mental retardation, atherosclerosis, and arthritis. Though cell motility has been studied for decades, and molecular basis of cell migration has progressed rapidly over the recently few years, there are still many unresolved issues regarding how cell maintain the polarity, how adhesions disperse, how cells recognize their targets, how components are integrated temporally and spatially across the cell. (*Science*, 302:1704.) Cell migration requires the participation of a dynamic and interactive actin cytoskeleton that acts to deform cellular membranes. Many factors have been reported to be concerned with these 'actin-based motility processes'.

Coronins are a conserved family of F-actin binding proteins that contain WD40 repeats. Yeast *Saccharomyces cerevisiae* and *Dictyostelium discoideum* each have a single gene encoding Coronin; but in mammals, this gene family has expanded to include seven genes: CORO1A, CORO1B, CORO1C, CORO1D, CORO2A, CORO2B and POD (based on the HGNC nomenclature).

Coro1B, first identified as a downstream target of PKC in 1999, is expressed in many tissue and cell lines. Some primary experiments show that Coro1B is localized to the region of dynamic actin at the leading edge and weakly along stress fibers, which indicates possible roles of Coro1B in actin dynamics and cell migration.



## RESULTS AND FUTURE WORKS

**Fig.4 Antibody tests**

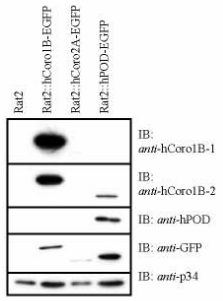



**Fig.5 Trial of hCoro1B IP**

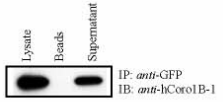



**Fig.6 Cell state influences the location of hCoro1B-EGFP**

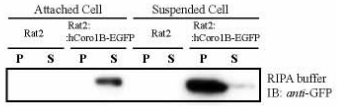
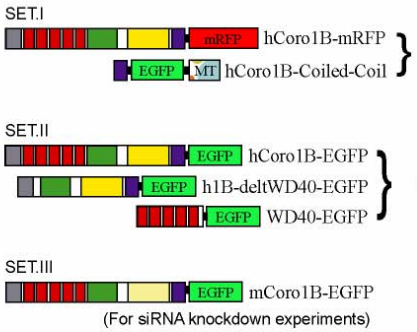
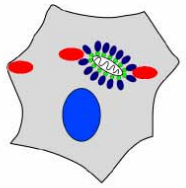



**Fig.7 Diagram of Retrovirus constructs**



How hCoro1B binds to actin?

## BIOINFORMATICS ANALYSIS

**Tab.1 Sequence similarity based on DNA$^{(upper)}$/amino acid$_{(lower)}$ data**

| | h1A | m1A | r1A |
|---|---|---|---|
| h1A | 1 | 0.83 | 0.83 |
| m1A | 0.94 | 1 | 0.96 |
| r1A | 0.94 | 0.99 | 1 |

| | h1B | m1B | r1B |
|---|---|---|---|
| h1B | 1 | 0.82 | 0.79 |
| m1B | 0.94 | 1 | 0.91 |
| r1B | 0.92 | 0.97 | 1 |

| | h2A | m2A |
|---|---|---|
| h2A | 1 | 0.51 |
| m2A | 0.85 | 1 |

| | h2B | m2B |
|---|---|---|
| h2B | 1 | 0.68 |
| m2B | 0.98 | 1 |

| | h1C | m1C |
|---|---|---|
| h1C | 1 | 0.69 |
| m1C | 0.97 | 1 |

| | h1D | m1D | r1D |
|---|---|---|---|
| h1D | 1 | 0.51 | 0.40 |
| m1D | 0.47 | 1 | 0.49 |
| r1D | 0.46 | 0.95 | 1 |

| | hPOD | mPOD | rPOD |
|---|---|---|---|
| hPOD | 1 | 0.64 | 0.52 |
| mPOD | 0.86 | 1 | 0.42 |
| rPOD | 0.37 | 0.40 | 1 |

**Fig.2 Phylogenetic tree of coronin family**

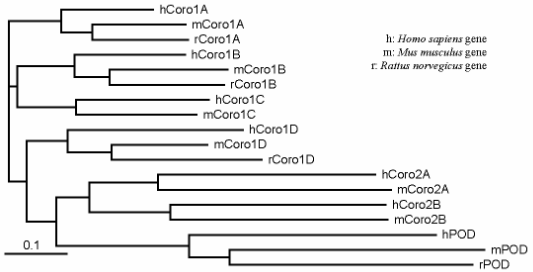



**Fig.1 CORO1B motif prediction**

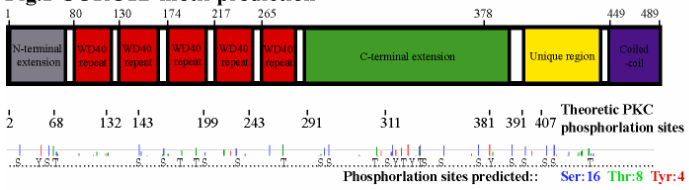
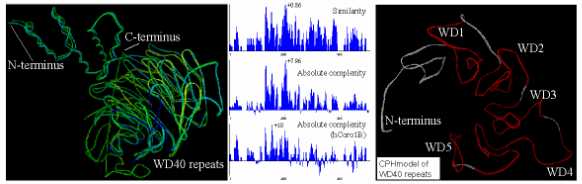



**Fig.3 hCoro1B 3-D structure predicted by SWISS-MODEL**

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